

# Pre-Processing Spectroscopic Data for Omics Analysis

**Dr. David M. Rocke**

University of California, Davis

Statistical Consulting Director candidate in  
Agricultural and Biosystems Engineering

**Thursday, March 6, 2008**

**12:00 pm**

**Bio Sciences West – Room 210**

**Abstract:**

Many methods of advanced biological measurement are spectroscopic in nature – in particular, mass spectrometry for proteomics and metabolomics and NMR spectroscopy for metabolomics. In order to perform statistical analysis for differences between groups, dose-response, etc., many different types of preprocessing are necessary. These include baseline correction, data transformation, spectral alignment, peak identification, and peak quantitation. We present methods and observations on statistically based approaches to this problem.

Questions: Dr. Walt Piegorsch, Mathematics, 621-2157, [wpiegors@email.arizona.edu](mailto:wpiegors@email.arizona.edu)